

## SEQUENCE LISTING

&lt;110&gt; SmithKline Beecham Biologicals

&lt;120&gt; Novel compounds

&lt;130&gt; BM45311

&lt;160&gt; 14

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Bacteria

&lt;400&gt; 1

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tacactgggg ttatctatac	tggtgttgca cctttggtag	ataatgatga gaccgttaag	180
gctctggcaa gcaagctacc	cagtttggtt tattttgact	ttgattctga tgagattaaa	240
ccgcaagctg ctgccatctt	agacgaacaa gcacaatttt	taaccaccaa tcaaacagct	300
cgtgttttgg ttgcaggcca	taccgatgag cgtggtagtc	gtgagtataa tatgtcactg	360
ggggaacgcc gtgcggtggc	ggtacgcaac tatttgcttg	gtaaaggcat taatcaagcc	420
agcggttgaga ttatcagttt	tggtgaagaa cgccctatcg	catttggcac aaatgaagaa	480
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&lt;210&gt; 2

&lt;211&gt; 172

&lt;212&gt; PRT

&lt;213&gt; Bacteria

&lt;400&gt; 2

Met Met Leu His Ile Gln Ile Ala Ala Ala Ala Ala Leu Ser Val

1

5

10

15

Leu Thr Phe Met Thr Gly Cys Ala Asn Lys Ser Thr Ser Gln Val Met  
 20 25 30  
 Val Ala Pro Asn Ala Pro Thr Gly Tyr Thr Gly Val Ile Tyr Thr Gly  
 35 40 45  
 Val Ala Pro Leu Val Asp Asn Asp Glu Thr Val Lys Ala Leu Ala Ser  
 50 55 60  
 Lys Leu Pro Ser Leu Val Tyr Phe Asp Phe Asp Ser Asp Glu Ile Lys  
 65 70 75 80  
 Pro Gln Ala Ala Ala Ile Leu Asp Glu Gln Ala Gln Phe Leu Thr Thr  
 85 90 95  
 Asn Gln Thr Ala Arg Val Leu Val Ala Gly His Thr Asp Glu Arg Gly  
 100 105 110  
 Ser Arg Glu Tyr Asn Met Ser Leu Gly Glu Arg Arg Ala Val Ala Val  
 115 120 125  
 Arg Asn Tyr Leu Leu Gly Lys Gly Ile Asn Gln Ala Ser Val Glu Ile  
 130 135 140  
 Ile Ser Phe Gly Glu Glu Arg Pro Ile Ala Phe Gly Thr Asn Glu Glu  
 145 150 155 160  
 Ala Trp Ser Gln Asn Arg Arg Ala Glu Leu Ser Tyr  
 165 170

&lt;210&gt; 3

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Bacteria

&lt;400&gt; 3

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 gctctagcaa gcacgctacc cagtttggtt tattttgact ttgattctga tgagattaaa 240  
 ccgcaagctg ctgccatctt agacgaacaa gcacaatttt taaccaccaa tcaaacagct 300  
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 agcgttgaga ttatcagttt tgggtgaagaa cgccctatcg catttggtcac aaatgaagaa 480  
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&lt;210&gt; 4

&lt;211&gt; 172

<213> Bacteria

<400> 4

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			20					25					30		
Val	Ala	Pro	Asn	Ala	Pro	Thr	Gly	Tyr	Thr	Gly	Val	Ile	Tyr	Thr	Gly
		35					40					45			
Val	Ala	Pro	Leu	Val	Asp	Asn	Asp	Glu	Thr	Val	Lys	Ala	Leu	Ala	Ser
	50					55				60					
Thr	Leu	Pro	Ser	Leu	Val	Tyr	Phe	Asp	Phe	Asp	Ser	Asp	Glu	Ile	Lys
65				70						75				80	
Pro	Gln	Ala	Ala	Ala	Ile	Leu	Asp	Glu	Gln	Ala	Gln	Phe	Leu	Thr	Thr
			85						90				95		
Asn	Gln	Thr	Ala	Arg	Val	Leu	Val	Ala	Gly	His	Thr	Asp	Glu	Arg	Gly
		100						105					110		
Ser	Arg	Glu	Tyr	Asn	Met	Ser	Leu	Gly	Glu	Arg	Arg	Ala	Val	Ala	Val
	115					120					125				
Arg	Asn	Tyr	Leu	Leu	Gly	Lys	Gly	Ile	Asn	Gln	Ala	Ser	Val	Glu	Ile
	130					135					140				
Ile	Ser	Phe	Gly	Glu	Glu	Arg	Pro	Ile	Ala	Phe	Gly	Thr	Asn	Glu	Glu
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Ala	Trp	Ser	Gln	Asn	Arg	Arg	Ala	Glu	Leu	Ser	Tyr				
			165					170							

<213> Bacteria

<400> 5

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actttggcaa	gcacgctacc	cagtttgggt	tattttgact	ttgattctga	tgagattaaa	240
ccgcaagctg	ctgccatctt	agacgaacaa	gcacaatttt	taaccaccaa	tcaaacagct	300
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ggggaacgcc gtgcggtggc ggtacgcaac tatttgcttg gtaaaggcat taatcaagcc 420
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gcatgggtcac aaaatcgctg tgctgaactg tcttattaa 519

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<210> 6  
 <211> 172  
 <212> PRT  
 <213> Bacteria

<400> 6

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Val Ala Pro Asn Ala Pro Thr Gly Tyr Thr Gly Val Ile Tyr Thr Gly
      35              40              45
Val Ala Pro Leu Val Asp Asn Asp Glu Thr Ile Lys Thr Leu Ala Ser
      50              55              60
Thr Leu Pro Ser Leu Val Tyr Phe Asp Phe Asp Ser Asp Glu Ile Lys
      65              70              75              80
Pro Gln Ala Ala Ala Ile Leu Asp Glu Gln Ala Gln Phe Leu Thr Thr
      85              90              95
Asn Gln Thr Ala Arg Val Leu Val Ala Gly His Thr Asp Glu Arg Gly
      100             105             110
Ser Arg Glu Tyr Asn Met Ser Leu Gly Glu Arg Arg Ala Val Ala Val
      115             120             125
Arg Asn Tyr Leu Leu Gly Lys Gly Ile Asn Gln Ala Ser Val Glu Ile
      130             135             140
Ile Ser Phe Gly Glu Glu Arg Pro Ile Ala Phe Gly Thr Asn Glu Glu
      145             150             155             160
Ala Trp Ser Gln Asn Arg Arg Ala Glu Leu Ser Tyr
      165             170

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<210> 7  
 <211> 519  
 <212> DNA  
 <213> Bacteria

<400> 7

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tacgctggcg ttatctacac tgggtgtgca cctttggtag ataatgatga gaccgtcaag      180
gctttggcaa gcacgctacc cagtttggtt tattttgact ttgattctga tgagattaaa      240
ccgcaagctg ctgccatctt agacgaacaa gcacaatttt taaccaccaa tcaaacagct      300
cgtgttttgg ttgcaggtea taccgatgag cgtggtagtc gtgagtataa tatgtcactg      360
ggggaacgcc gtgcggtggc ggtacgcaac tatttgctta gtaaaggcat caatcaagcc      420
agcgttgaga ttatcagttt tgggtgaagaa cgccctatcg catttggcac aaatgaagaa      480
gcatggtcac aaaatcgtcg tgctgaactg tcttattaa      519

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&lt;210&gt; 8

&lt;211&gt; 172

&lt;212&gt; PRT

&lt;213&gt; Bacteria

&lt;400&gt; 8

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Met Met Leu His Ile Gln Ile Ala Ala Ala Ala Ala Leu Ser Val
  1             5             10             15
Leu Thr Phe Met Thr Gly Cys Ala Asn Lys Ser Thr Ser Gln Val Met
      20             25             30
Val Ala Pro Asn Ala Pro Thr Gly Tyr Ala Gly Val Ile Tyr Thr Gly
      35             40             45
Val Ala Pro Leu Val Asp Asn Asp Glu Thr Val Lys Ala Leu Ala Ser
      50             55             60
Thr Leu Pro Ser Leu Val Tyr Phe Asp Phe Asp Ser Asp Glu Ile Lys
      65             70             75             80
Pro Gln Ala Ala Ala Ile Leu Asp Glu Gln Ala Gln Phe Leu Thr Thr
      85             90             95
Asn Gln Thr Ala Arg Val Leu Val Ala Gly His Thr Asp Glu Arg Gly
      100            105            110
Ser Arg Glu Tyr Asn Met Ser Leu Gly Glu Arg Arg Ala Val Ala Val
      115            120            125
Arg Asn Tyr Leu Leu Ser Lys Gly Ile Asn Gln Ala Ser Val Glu Ile
      130            135            140
Ile Ser Phe Gly Glu Glu Arg Pro Ile Ala Phe Gly Thr Asn Glu Glu
      145            150            155            160
Ala Trp Ser Gln Asn Arg Arg Ala Glu Leu Ser Tyr
      165            170

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<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence

<400> 9

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21

<210> 10

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence

<400> 10

ggcagagtga atcttaagc

19

<210> 11

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide

<400> 11

aagggcccaa ttacgcagag gggatccaat aaatcaacaa gtcaagttat gggtgctcc 59

<210> 12

<211> 65

<212> DNA

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide

&lt;400&gt; 12

aagggcccaa ttacgcagag ggtcgactta ttaataagac agttcagcac gacgattttg tgacc 65

&lt;210&gt; 13

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; peptide

&lt;400&gt; 13

Cys Asn Glu Glu Ala Trp Ser Gln Asn Arg Arg Ala Glu Leu Ser Tyr

1

5

10

15

&lt;210&gt; 14

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; peptide

&lt;400&gt; 14

Tyr Thr Gly Val Ala Pro Leu Val Asp Asn Asp Glu Thr Val

1

5

10

## SEQUENCE INFORMATION

## BASB019 Polynucleotide and Polypeptide Sequences

## SEQ ID NO:1

*Moraxella catarrhalis* BASB019 polynucleotide sequence from strain MC2931

ATGATGTTACATATTCAAATTGCCGCCGCTGCCGCCGCTTTATCGGTACTAACTTTTAT  
GACAGGCTGTGCCAATAAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACAG  
GTTACACTGGGGTTATCTATACTGGTGTGTCACCTTTGGTAGATAATGATGAGACCGTT  
AAGGCTCTGGCAAGCAAGCTACCCAGTTTGGTTTATTTTGACTTTGATTCTGATGAGAT  
TAAACCGCAAGCTGCTGCCATCTTAGACGAACAAGCACAATTTTAAACCACCAATCAAA  
CAGCTCGTGTGTTTGGTTGCAGGTCATACCGATGAGCGTGGTAGTCGTGAGTATAATATG  
TCACTGGGGGAACGCCGTGCGGTGGCGGTACGCAACTATTTGCTTGGTAAAGGCATTAA  
TCAAGCCAGCGTTGAGATTATCAGTTTGGTGAAGAACGCCCTATCGCATTTGGCACAA  
ATGAAGAAGCATGGTCACAAAATCGTCGTGCTGAACTGTCTTATTAA

## SEQ ID NO:2

*Moraxella catarrhalis* BASB019 polypeptide sequence from strain MC2931

MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDET  
KALASKLPSLVYDFDSDSEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM  
SLGERRAVAVRNYLLGKGINQASVEIISFGEERPFAFGTNEEAWSQNRRAELSY

## SEQ ID NO:3

*Moraxella catarrhalis* BASB019 polynucleotide sequence from strain Mcat 2911

ATGATGTTACATATTCAAATTGCCGCCGCTGCCGCCGCTTTATCGGTACTAACTTTTAT  
GACAGGCTGTGCCAATAAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACAG  
GTTACACTGGGGTTATCTATACTGGTGTGTCACCTTTGGTAGATAATGATGAGACCGTT  
AAGGCTCTAGCAAGCACGCTACCCAGTTTGGTTTATTTTGACTTTGATTCTGATGAGAT  
TAAACCGCAAGCTGCTGCCATCTTAGACGAACAAGCACAATTTTAAACCACCAATCAAA  
CAGCTCGTGTGTTTGGTTGCAGGTCATACCGATGAGCGTGGTAGTCGTGAGTATAATATG  
TCACTGGGGGAACGTCGTGCGGTGGCGGTACGCAACTATTTGCTTGGTAAAGGCATTAA  
TCAAGCCAGCGTTGAGATTATCAGTTTGGTGAAGAACGCCCTATCGCATTTGGCACAA  
ATGAAGAAGCATGGTCACAAAATCGTCGTGCTGAACTGTCTTATTAA

## SEQ ID NO:4

*Moraxella catarrhalis* BASB019 polypeptide sequence from strain Mcat 2911



MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDET  
KALASTLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM  
SLGERRAVAVRNYLLGKGINQASVEIISFGEERPPIAFGTNEEAWSQNRRAELSY

**SEQ ID NO:5**

*Moraxella catarrhalis* BASB019 polynucleotide sequence from strain Mcat 2960

ATGATGTTACATATTCAAATTGCCGCCGCTGCCGCCGCTTTATCGGTACTAACTTTTAT  
GACAGGCTGTGCCAATAAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACAG  
GTTACACTGGGGTTATCTATACTGGTGTTCACCTTTGGTAGATAATGATGAGACTATC  
AAGACTTTGGCAAGCACGCTACCCAGTTTGGTTTATTTTGACTTTGATTCTGATGAGAT  
TAAACCGCAAGCTGCTGCCATCTTAGACGAACAAGCACAATTTTAAACCACCAATCAAA  
CAGCTCGTGTTTTGGTTGCAGGTCATACCGATGAGCGTGGTAGTCGTGAGTATAATATG  
TCACTGGGGGAACGCCGTGCGGTGGCGGTACGCAACTATTTGCTTGGTAAAGGCATTAA  
TCAAGCCAGCGTTGAGATTATCAGTTTTGGTGAAGAACGCCCTATCGCATTTGGCACAA  
ATGAAGAAGCATGGTCACAAAATCGTCGTGCTGAACTGTCTTATTAA

**SEQ ID NO:6**

*Moraxella catarrhalis* BASB019 polypeptide sequence from strain Mcat 2960

MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYTGVIYTGVAPLVDNDETI  
KTLASTLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM  
SLGERRAVAVRNYLLGKGINQASVEIISFGEERPPIAFGTNEEAWSQNRRAELSY

**SEQ ID NO:7**

*Moraxella catarrhalis* BASB019 polynucleotide sequence from strain Mcat 2969

ATGATGTTACATATTCAAATTGCCGCTGCTGCCGCCGCTTTATCGGTACTAACTTTTAT  
GACAGGCTGTGCCAATAAATCAACAAGTCAAGTTATGGTTGCTCCTAATGCACCCACGG  
GTTACGCTGGCGTTATCTACACTGGTGTTCACCTTTGGTAGATAATGATGAGACCGTC  
AAGGCTTTGGCAAGCACGCTACCCAGTTTGGTTTATTTTGACTTTGATTCTGATGAGAT  
TAAACCGCAAGCTGCTGCCATCTTAGACGAACAAGCACAATTTTAAACCACCAATCAAA  
CAGCTCGTGTTTTGGTTGCAGGTCATACCGATGAGCGTGGTAGTCGTGAGTATAATATG  
TCACTGGGGGAACGCCGTGCGGTGGCGGTACGCAACTATTTGCTTAGTAAAGGCATCAA  
TCAAGCCAGCGTTGAGATTATCAGTTTTGGTGAAGAACGCCCTATCGCATTTGGCACAA  
ATGAAGAAGCATGGTCACAAAATCGTCGTGCTGAACTGTCTTATTAA

**SEQ ID NO:8**

*Moraxella catarrhalis* BASB019 polypeptide sequence from strain Mcat 2969

MMLHIQIAAAAAALSVLTFMTGCANKSTSQVMVAPNAPTGYAGVIYTGVAPLVDNDETV  
KALASTLPSLVYFDFDSDEIKPQAAAILDEQAQFLTTNQTARVLVAGHTDERGSREYNM  
SLGERRAVAVRNYLLSKGINQASVEIISFGEERPPIAFGTNEEAWSQNRRAELSY

**SEQ ID NO:9**

CCC TTA TTA ATT GAC AAT CAC

**SEQ ID NO:10**

GGC AGA GTG AAT CTT AAG C

**SEQ ID NO:11**

AAG GGC CCA ATT ACG CAG AGG GGA TCC AAT AAA TCA ACA AGT CAA  
GTT ATG GTT GCT CC

**SEQ ID NO:12**

AAG GGC CCA ATT ACG CAG AGG GTC GAC TTA TTA ATA AGA CAG TTC  
AGC ACG ACG ATT TTG TGA CC

**SEQ ID NO:13**

CNEEAWSQNRRAELSY

**SEQ ID NO:14**

YTGVAPLVDNDETV